

SEQUENCE LISTING

<110> Allen, Steve
Kinney, Tony
Miao, Gou-Hua
Orozco, Buddy

<120> PLANT BIOTIN SYNTHASE

<130> BB1429 US NA

<140>

<141>

<150> 60/172929

<151> December 21, 1999

<160> 36

<170> Microsoft Office 97

<210> 1

<211> 512

<212> DNA

<213> Hordeum vulgare

<220>

<221> unsure

<222> (94)

<220>

<221> unsure

<222> (460)

<220>

<221> unsure

<222> (462)

<400> 1

```
caactccctc ggcagtatcg cctagtgcag cagcggctcc gttccggcca gctttgctcg 60
ccgagccggc catgatgctg ctgctcgcgc gcancttcgc tcccgcgtcc ggtccccctt 120
cgcctccgcc gttagcgccg cgcccttctc atcggtatcg gcggccgcgg cggaggcggg 180
cgggcgggtgc gggacggggc caggaacgac tggaccgcgc ccgagatcca ggccatctac 240
gactccccgc tctctgacct cctcttccac ggggctcaag tccataggaa tgtccataaa 300
tttagagaag tgcaacaatg cacacttctt tcaataaaga ctggtgggtg cagcgaagat 360
tgttcatact gcccacagtc ttcaagatac agtaccggat tgaaggctga aaaattaatg 420
aagaaagatg ccgtcctaga agcagctaaa aaggcaaagn angctgggag cacccgattt 480
tgattggagc gatggagaga gacaattggc ag 512
```

<210> 2

<211> 137

<212> PRT

<213> Hordeum vulgare

<220>

<221> UNSURE

<222> (131)


```

ggggntcagt catcaagata caacactgga ttgaagggcc aaaaattgat gaacaaatat 420
gctgtcttgg gagcagcaaa aaaggnaaaa gagtctggga agcaaccgtt tttgcatggg 480
aactgcattg gagaaa                                         496

```

```

<210> 4
<211> 102
<212> PRT
<213> Zea mays

```

```

<220>
<221> UNSURE
<222> (48)..(49)

```

```

<220>
<221> UNSURE
<222> (64)

```

```

<220>
<221> UNSURE
<222> (91)

```

```

<400> 4
Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
 1              5              10              15
Pro Leu Ala Ala Ala Ala Gly Phe Ser Ser Ala Ala Ala Glu Ala Glu
      20              25              30
Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Xaa
      35              40              45
Xaa Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Xaa
      50              55              60
Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Gly Gln Lys Leu Met Asn
      65              70              75              80
Lys Tyr Ala Val Leu Gly Ala Ala Lys Lys Xaa Lys Glu Ser Gly Lys
      85              90              95
Gln Pro Phe Leu His Gly
      100

```

```

<210> 5
<211> 497
<212> DNA
<213> Zea mays

```

```

<220>
<221> unsure
<222> (192)

```

```

<220>
<221> unsure
<222> (460)

```

```

<220>
<221> unsure
<222> (463)

```

<220>
 <221> unsure
 <222> (469)

<220>
 <221> unsure
 <222> (490)

<400> 5
 agccgacgag gcgaggagcg tgcaattccg tagctgcaac tgcaacgaac tccctccctc 60
 cctcgaccgt atcgcccgt gtcctctat ccccttctctg ctgctgctac taccttaagc 120
 tatcatggcc ttgatgctgc tagcgcgcaa cctgcgctcc cgcctccgcc caccgctcgc 180
 cgccgcccgc gngttctcgt cggccgcggc ggaggcggag agggcgatac gggacgggcc 240
 gcggaacgac tggagccggc ccgagattca agccgtctac gactcaccgc tcctcgacct 300
 cctctttcac ggggctcaag tccacagaaa tgtccataaa ttcaagagaa gtgcagcaat 360
 gcacacttct ttcaatcaag actggtggga tgcagtgaag attgttctta ctgtcctcaa 420
 gtcatacaag aatacaacac tgggattgaa gggcccaaan aanttgatna acaaaagatg 480
 ctgtcttggn aacaaca 497

<210> 6
 <211> 98
 <212> PRT
 <213> Zea mays

<220>
 <221> UNSURE
 <222> (23)

<220>
 <221> UNSURE
 <222> (72)

<220>
 <221> UNSURE
 <222> (89)

<400> 6
 Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
 1 5 10 15
 Pro Leu Ala Ala Ala Ala Xaa Phe Ser Ser Ala Ala Ala Glu Ala Glu
 20 25 30
 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
 35 40 45
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
 50 55 60
 Gln Val His Arg Asn Val His Xaa Ser Arg Glu Val Gln Gln Cys Thr
 65 70 75 80
 Leu Leu Ser Ile Lys Thr Gly Gly Xaa Ser Glu Asp Cys Ser Tyr Cys
 85 90 95
 Pro Gln

<210> 7
 <211> 1152

<212> DNA
 <213> Zea mays

<400> 7
 gcagccgacg aggcgaggag cgtgcaattc cgtagctgca acgaactccc tcgaccgtat 60
 cgcccgtgc tcctctatcc ctttcctgct gctgctacta ccttaagcta tcactatcat 120
 ggccttgatg ctgctagcgc gcaacctgcg ctcccgcctc cgcccaccgc tcgccgccgc 180
 cgcggcggtc tcgtcggccg cggcggaggc ggagagggcg atacgggacg ggccgcggaa 240
 cgactggagc cggcccgaga tccaggccgt ctacgactca ccgctcctcg acctcctctt 300
 tcacggggct cagggtccaca gaaatgtcca taaattcaga gaagtgcagc aatgcacact 360
 tctttcaatc aagactgggtg gatgcagtga agattgttct tactgtcctc agtcatcaag 420
 atacaacact ggattgaagg cccaaaaatt gatgaacaaa tatgctgtct tggaagcagc 480
 aaaaaaggca aaagagtctg ggagcaccgc tttttgcatg ggagctgcat ggagagaaac 540
 cattggcagg aatcaaaact tcaaccagat tcttgaatat gtcaaggaaa taaggggtat 600
 gggcatggag gtctgttgca cactaggcat gatagagaaa caacaagctg aagaactcaa 660
 gaaggctgga cttacagcat ataatacataa cctagatata tcaagagagt attatcccaa 720
 cattattacc acaagatcat atgatgatag actgcagact cttgagcatg tccgtgaagc 780
 tggaataagc atctgctcag gtggaatcat tgggtcttggg gaagcagagg aggaccgggt 840
 agggttgttg cataccctag ctaccttgcc tacacaccca gagagcgttc ctattaatgc 900
 attggttgct gtaaaaggca cacctcttga ggaccagaag cctgtagaga tctgggaaat 960
 gatccgcagt atcgccactg ctcggatcac gatgccaaag gcaatggtga ggctttcagc 1020
 aggccgagta cggttctcga tgccagaaca agcgtgtgct ttctcgtctg gggccaactc 1080
 catccttgcc ggcgagaaac ttctcacaac cgcaaacaac gactttgatg cggaccaagc 1140
 gatgttcaag at 1152

<210> 8
 <211> 344
 <212> PRT
 <213> Zea mays

<400> 8
 Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
 1 5 10 15
 Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
 20 25 30
 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
 35 40 45
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
 50 55 60
 Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
 65 70 75 80
 Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
 85 90 95
 Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
 100 105 110
 Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly
 115 120 125
 Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
 130 135 140
 Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly
 145 150 155 160

Met	Gly	Met	Glu	Val	Cys	Cys	Thr	Leu	Gly	Met	Ile	Glu	Lys	Gln	Gln	
				165					170					175		
Ala	Glu	Glu	Leu	Lys	Lys	Ala	Gly	Leu	Thr	Ala	Tyr	Asn	His	Asn	Leu	
				180					185					190		
Asp	Thr	Ser	Arg	Glu	Tyr	Tyr	Pro	Asn	Ile	Ile	Thr	Thr	Arg	Ser	Tyr	
				195					200					205		
Asp	Asp	Arg	Leu	Gln	Thr	Leu	Glu	His	Val	Arg	Glu	Ala	Gly	Ile	Ser	
				210					215					220		
Ile	Cys	Ser	Gly	Gly	Ile	Ile	Gly	Leu	Gly	Glu	Ala	Glu	Glu	Asp	Arg	
				225					230					235		
Val	Gly	Leu	Leu	His	Thr	Leu	Ala	Thr	Leu	Pro	Thr	His	Pro	Glu	Ser	
				245					250					255		
Val	Pro	Ile	Asn	Ala	Leu	Val	Ala	Val	Lys	Gly	Thr	Pro	Leu	Glu	Asp	
				260					265					270		
Gln	Lys	Pro	Val	Glu	Ile	Trp	Glu	Met	Ile	Arg	Met	Ile	Ala	Thr	Ala	
				275					280					285		
Arg	Ile	Thr	Met	Pro	Lys	Ala	Met	Val	Arg	Leu	Ser	Ala	Gly	Arg	Val	
				290					295					300		
Arg	Phe	Ser	Met	Pro	Glu	Gln	Ala	Leu	Cys	Phe	Leu	Ala	Gly	Ala	Asn	
				305					310					315		
Ser	Ile	Leu	Ala	Gly	Glu	Lys	Leu	Leu	Thr	Thr	Ala	Asn	Asn	Asp	Phe	
				325					330					335		
Asp	Ala	Asp	Gln	Ala	Met	Phe	Lys									
				340												

```
<210> 9
<211> 562
<212> DNA
<213> Argemone mexicana
```

<400>	9					
cattcgagaa	ataaagagct	gtaaaatttt	taggggtttt	ctgcataact	ctacactcga	60
agcttcatca	atagaaatat	cataaacaga	agaattcaaa	atgcttaaag	ttcaatcttt	120
gagagctcgt	cttcgacctt	tgattttcat	ttctacattt	tcttctctct	catcatcttc	180
ttcttcttca	gctgctgctg	ttcaagcaga	agaacgatt	aaagaagggtc	caagaaacga	240
ttggagcaga	gatgaaatta	aatcggttta	tgattctcca	gttctcgatc	ttctcttcca	300
tgcagctcaa	gtccatagac	atgctcacaa	cttcagggaa	gtgcagcaat	gtactcttct	360
ctctgttaag	acagggtgggt	gcagtgaaga	ttgttcatat	tgtcacacaat	cttcaggtta	420
tgacactgga	gtgaaagccc	aaaagctgat	gaacaaggga	cgcagttctg	caaggaagca	480
agaaaaggca	aaggagggcg	ggtagtacac	gttttcgcaa	tggtggctgc	aatggggaga	540
tacaatgggg	aanqaagaac	aa				562

<212> PRT
 <213> Argemone mexicana

<400> 10
 Met Leu Lys Val Gln Ser Leu Arg Ala Arg Leu Arg Pro Leu Ile Phe
 1 5 10 15
 Ile Ser Thr Phe Ser Ser Leu Ser Ser Ser Ser Ser Ser Ala Ala
 20 25 30
 Ala Val Gln Ala Glu Arg Thr Ile Lys Glu Gly Pro Arg Asn Asp Trp
 35 40 45
 Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu
 50 55 60
 Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu
 65 70 75 80
 Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu
 85 90 95
 Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys
 100 105 110
 Ala Gln Lys Leu Met Asn Lys
 115

<210> 11
 <211> 1340
 <212> DNA
 <213> Glycine max

<400> 11
 ctagtactgc tccctctgcg acttcgtttc gtagagggat tttggccgcc aaataaacag 60
 tctcaccata aactccaaag tcccaacgct aaacgaaacc aaaccccaaa cacaataacc 120
 gttgttgtct gttgtctctg tcgtgtctat attcgcagat ctctcactca ttctctgttg 180
 tttctctgcc caacttcgaa ttcgaaagca aaaacatggt tttggcgaga cccattttcc 240
 gagcaccctc cctttgggcg ttgcactctt cctacgcgta ttctctgcc tcagcagctg 300
 caattcaagc tgagagagcc atcaaagaag gaccagaaaa cgattggagc cgagaccaag 360
 tcaaatccat ctacgactct cccattctcg atcttctctt ccatggggct caagttcaca 420
 gacatgctca taacttcagg gaagttcaac agtggtactct tctgtctatc aaaacaggag 480
 ggtgcagtga agattgttcc tattgtcctc aatcctctaa gtatgataca ggagtcaaaa 540
 ggccaagcct tatgaacaag gaagctgttc tccaggctgc aaagaaggca aaagaggctg 600
 ggagcactcg cttttgtatg ggtgctgctg ggaggggatac actaggaaga aagaccaact 660
 tcaaccagat ccttgaatat gtgaaagaca taagggacat ggggaatggag gtttggttgca 720
 cccttggcat gctggagaaa cagcaggctg ttgaactcaa gaaggcagggt ctactgctt 780
 ataatcacia tcttgacact tcaagggagt attatccaaa cataatcaca acaaggactt 840
 atgatgagcg tcttcaaacc cttaggtttg ttcgggatgc agggatcaat gtttgttctg 900
 gaggaattat agggcttgga gaagcagagg aggatcgtgt aggtttgtta catacattgt 960
 caacacttcc caccatcca gagagtgttc ctattaatgc acttgttgct gtaaagggaa 1020
 cccctcttga ggatcagaag cctgttgaaa tatgggagat gattcgcagt atagcaactg 1080
 cacgtatcgt aatgccaaaa gcaatggtea ggttatcagc tggcagagtt cgattctcca 1140
 tgcttgagca ggcattgtgc tttcttgctg gtgcaaatc tatattcact ggtgaaaagc 1200
 ttctcactac tcctaacaat gattttgatg ctgatcaact catgtttaaa gttcttggac 1260
 ttctcccaaa agctccaagc ttacatgaag gtgaaactag tgtgacagaa gattataagg 1320
 aagcagcttc ttctagttga 1340

<210> 12
 <211> 374

<212> PRT
 <213> Glycine max

<400> 12

```

Met Phe Leu Ala Arg Pro Ile Phe Arg Ala Pro Ser Leu Trp Ala Leu
 1             5             10             15

His Ser Ser Tyr Ala Tyr Ser Ser Ala Ser Ala Ala Ala Ile Gln Ala
 20             25             30

Glu Arg Ala Ile Lys Glu Gly Pro Arg Asn Asp Trp Ser Arg Asp Gln
 35             40             45

Val Lys Ser Ile Tyr Asp Ser Pro Ile Leu Asp Leu Leu Phe His Gly
 50             55             60

Ala Gln Val His Arg His Ala His Asn Phe Arg Glu Val Gln Gln Cys
 65             70             75             80

Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr
 85             90             95

Cys Pro Gln Ser Ser Lys Tyr Asp Thr Gly Val Lys Arg Pro Ser Leu
100             105             110

Met Asn Lys Glu Ala Val Leu Gln Ala Ala Lys Lys Ala Lys Glu Ala
115             120             125

Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Asp Thr Leu Gly
130             135             140

Arg Lys Thr Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg
145             150             155             160

Asp Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln
165             170             175

Gln Ala Val Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn
180             185             190

Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Thr
195             200             205

Tyr Asp Glu Arg Leu Gln Thr Leu Glu Phe Val Arg Asp Ala Gly Ile
210             215             220

Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp
225             230             235             240

Arg Val Gly Leu Leu His Thr Leu Ser Thr Leu Pro Thr His Pro Glu
245             250             255

Ser Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu
260             265             270

Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr
275             280             285

Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg
290             295             300

```


Val Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala
 305 310 315 320

Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr Pro Asn Asn Asp
 325 330 335

Phe Asp Ala Asp Gln Leu Met Phe Lys Val Leu Gly Leu Leu Pro Lys
 340 345 350

Ala Pro Ser Leu His Glu Gly Glu Thr Ser Val Thr Glu Asp Tyr Lys
 355 360 365

Glu Ala Ala Ser Ser Ser
 370

<210> 13
 <211> 479
 <212> DNA
 <213> Glycine max

<400> 13
 ggcgactctc agaacttccc tatcacgata cctcatcctc cttegctcca ataccacctaa 60
 actcgacact atctcttctt ctgttcgtct tcaagttcaa aagtcgagaa actatgggtac 120
 cgtatcatct gttcctcctc aagctacaga aacatcaagc acatcaccta gtaaggatgt 180
 ctaccaagaa gcactcaacg caactgaacc ccgcagcaat tggacaagag aagaaatcaa 240
 ggcgatctat gataagccat tgatggagtt atgttggggg gctggtagtt tgcacaggaa 300
 attccatata cctgggggcta ttcagatgtg tacattgttg aacatcaaga cgggtggttg 360
 ctcgaggagg ttgttcttac tggcgcccaa tcatcccgct accaaaccgg tctcaaagcc 420
 ctccaaaaat ggtcctccgt cgaatctgtc ctcgcaagcc gccccgcata gccaaaaga 479

<210> 14
 <211> 52
 <212> PRT
 <213> Glycine max

<400> 14
 Arg Ser Asn Trp Thr Arg Glu Glu Ile Lys Ala Ile Tyr Asp Lys Pro
 1 5 10 15

Leu Met Glu Leu Cys Trp Gly Ala Gly Ser Leu His Arg Lys Phe His
 20 25 30

Ile Pro Gly Ala Ile Gln Met Cys Thr Leu Leu Asn Ile Lys Thr Gly
 35 40 45

Gly Cys Ser Glu
 50

<210> 15
 <211> 589
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (321)

<220>
 <221> UNSURE
 <222> (69)

<400> 16
 Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr
 1 5 10 15

Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys Thr
 20 25 30

Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly Met Gly
 35 40 45

Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Glu
 50 55 60

Glu Leu Gln Glu Xaa Asp Phe Thr Ala Tyr Asn His Asn Leu
 65 70 75

<210> 17
 <211> 1396
 <212> DNA
 <213> Hordeum vulgare

<400> 17
 gcaccacaac tccctcggca gtatcgcccta gtgcagcagc ggctccggtc cggccagctt 60
 tgctcgccga gccggccatg atgctgctgc tcgcgcgcag ccttcgctcc cgcgtccggt 120
 ccccttcgc ctccgcggtt agcgccgcgc ccttctcatc ggtatcggcg gccgcggcgg 180
 aggcggagcg ggcggtgcgg gacgggcccga ggaacgactg gaccgcgcc gagatccagg 240
 ccatctacga ctccccgctc ctcgacctcc tcttccacgg ggctcaagtc cataggaatg 300
 tccataaatt tagagaagtg caacaatgca cacttctttc aataaagact ggtgggtgca 360
 gcgaagattg ttcatactgc ccacagtctt caagatacag taccggattg aaggctgaaa 420
 aattaatgaa gaaagatgcc gtcctagaag cagctaaaaa ggcaaaggag gctgggagca 480
 cccgattttg catgggagcc gcatggagag agacaattgg caggaaaaca aacttcaacc 540
 agattcttga atatgtcaag gacataagag gtatgggcat ggaggtctgt tgcaccctgg 600
 gcatgctaga gaaacagcaa gctgaagaac tcaagaaggc tggacttaca gcttataatc 660
 ataacctaga tacatcaaga gaatattacc cgaacattat ttctacaaga tcgtatgatg 720
 atagattaca gactcttcag catgtccgtg aagctggaat aagcgtctgc tcaggtggaa 780
 ttattggtct tggagaggcg gaggaagacc gtgtagggct gttgcataca ctggccactt 840
 tgccaacaca cccagagagt gttcctatca atgcattgat tgctgtcaaa ggcacgcctc 900
 ttcaggatca gaagcctgta gagatatggg aaatgatccg catgattgcc agcgcctcga 960
 ttgtgatgcc aaaggcaatg gtgagacttt cggcaggcg agtacgggtt tccatgccag 1020
 agcaagctct ctgctttctt gctggggcca actcgatctt cgccggtgaa aagctcctga 1080
 caactgcaaa caacgacttt gatgcggacc aggcaatgtt caagatcctt ggctgattc 1140
 ccaaggcacc gaactttggc gatgaggagg ccaccgtggc atcatccacg gagagatgtg 1200
 agcaagccgc ttcgatgtaa aatgttggtg tagattctcg agaccacatc cggtgcaaaa 1260
 ctggcaccat tatctccagc tagagctttg tactgtaggg atcatgatat tttgtactcc 1320
 ctccgttcct aaatataagt cttttaagcg atttcaaaaa aaaaaaaaaa aaaaaaaaaa 1380
 aaaaaaaaaa aaaaaa 1396

<210> 18
 <211> 405
 <212> PRT
 <213> Hordeum vulgare

<400> 18
 Thr Thr Thr Pro Ser Ala Val Ser Pro Ser Ala Ala Ala Pro Phe
 1 5 10 15

Arg Pro Ala Leu Leu Ala Glu Pro Ala Met Met Leu Leu Leu Ala Arg
 20 25 30
 Ser Leu Arg Ser Arg Val Arg Ser Pro Phe Ala Ser Ala Val Ser Ala
 35 40 45
 Ala Pro Phe Ser Ser Val Ser Ala Ala Ala Ala Glu Ala Glu Arg Ala
 50 55 60
 Val Arg Asp Gly Pro Arg Asn Asp Trp Thr Arg Pro Glu Ile Gln Ala
 65 70 75 80
 Ile Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala Gln Val
 85 90 95
 His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr Leu Leu
 100 105 110
 Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys Pro Gln
 115 120 125
 Ser Ser Arg Tyr Ser Thr Gly Leu Lys Ala Glu Lys Leu Met Lys Lys
 130 135 140
 Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr
 145 150 155 160
 Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys Thr
 165 170 175
 Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly Met Gly
 180 185 190
 Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Glu
 195 200 205
 Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr
 210 215 220
 Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Ser Thr Arg Ser Tyr Asp Asp
 225 230 235 240
 Arg Leu Gln Thr Leu Gln His Val Arg Glu Ala Gly Ile Ser Val Cys
 245 250 255
 Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val Gly
 260 265 270
 Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser Val Pro
 275 280 285
 Ile Asn Ala Leu Ile Ala Val Lys Gly Thr Pro Leu Gln Asp Gln Lys
 290 295 300
 Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Ser Ala Arg Ile
 305 310 315 320
 Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg Phe
 325 330 335

Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser Ile
340 345 350

Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe Asp Ala
355 360 365

Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala Pro Asn
370 375 380

Phe Gly Asp Glu Glu Ala Thr Val Ala Ser Ser Thr Glu Arg Cys Glu
385 390 395 400

Gln Ala Ala Ser Met
405

<210> 19
<211> 1467
<212> DNA
<213> Zea mays

<400> 19

gcacgagtc	aatcgggtg	cagtttttaa	ggaaaccagg	gaccgcagca	gcaagccgcc	60
ccagccgacg	aggcgaggag	cgtgcaattc	cgtagctgca	acgaactccc	tcgaccgtat	120
cgcccgtgc	tcctctatcc	ctttcctgct	gctgctacta	ccttaagcta	tcactatcat	180
ggccttgatg	ctgctagcgc	gcaacctgcg	ctccgcctc	cgcccaccgc	tcgccgccgc	240
cgcggcgttc	tcgtcggccg	cggcggaggc	ggagagggcg	atacgggacg	ggccgcggaa	300
cgactggagc	cggcccagaga	tccaggccgt	ctacgactca	ccgctcctcg	acctcctctt	360
tcacggggct	cagtcatcaa	gatacaaac	tggattgaag	gccccaaaaat	tgatgaacaa	420
atatgctgtc	ttggaagcag	caaaaaaggc	aaaagagtct	gggagcacc	gtttttgcat	480
gggagctgca	tggagagaaa	ccattggcag	gaaatcaaac	ttcaaccaga	ttcttgaata	540
tgtcaaggaa	ataaggggta	tgggcatgga	ggctctgttg	acactaggca	tgatagagaa	600
acaacaagct	gaagaactca	agaaggctgg	acttacagca	tataatcata	acctagatac	660
atcaagagag	tattatccca	acattattac	cacaagatca	tatgatgata	gactgcagac	720
tcttgagcat	gtccgtgaag	ctggaataag	catctgctca	ggtggaatca	ttggtcttgg	780
tgaagcagag	gaggaccggg	tagggttggt	gcatacccta	gctaccttgc	ctacacaccc	840
agagagcggt	cctattaatg	cattggttgc	tgtaaaaggc	acacctcttg	aggaccagaa	900
gcctgtagag	atctgggaaa	tgatccgc	gatcgccact	gctcggatca	cgatgccaaa	960
ggcaatgggt	aggctttcag	caggccgagt	acggttctcg	atgccagaac	aagcgctgtg	1020
cttcctcgct	ggggccaact	ccatctttgc	cggcgagaaa	cttctcacaa	ccgcaaacia	1080
cgactttgat	gcgaccagg	cgatgttcaa	gatccttggc	ctgatcccca	aggctccaag	1140
ctttggcgag	gaagaggcgt	ctgcggcggc	tcccacagaa	tccgagaggt	ctgagcaagc	1200
tgcttcgatg	tagaatatat	acatatcatt	accgattatc	cgtatcacgg	ttggggcgaa	1260
actagaacta	ccgtttagc	tagagcattg	gattgtagaa	accacaacat	ttcattat	1320
tgtaattgct	tgagactgaa	tgggggatac	ccatgtcggg	ctagatcaat	ggacaacttc	1380
cacacaacca	aatccaaaca	ttgaaactca	tttttcatca	cagttttaat	aaacttctcc	1440
cacttatctt	aaaaaaaaaa	aaaaaaa				1467

<210> 20
<211> 344
<212> PRT
<213> Zea mays

<400> 20

Met	Ala	Leu	Met	Leu	Leu	Ala	Arg	Asn	Leu	Arg	Ser	Arg	Leu	Arg	Pro
1				5					10				15		

Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
20 25 30

Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
 35 40 45
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
 50 55 60
 Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met Asn
 65 70 75 80
 Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly Ser
 85 90 95
 Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys
 100 105 110
 Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly Met
 115 120 125
 Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln Ala
 130 135 140
 Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp
 145 150 155 160
 Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr Asp
 165 170 175
 Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser Ile
 180 185 190
 Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val
 195 200 205
 Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser Val
 210 215 220
 Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp Gln
 225 230 235 240
 Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala Arg
 245 250 255
 Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg
 260 265 270
 Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser
 275 280 285
 Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe Asp
 290 295 300
 Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala Pro
 305 310 315 320
 Ser Phe Gly Glu Glu Glu Ala Ser Ala Ala Ala Pro Thr Glu Ser Glu
 325 330 335
 Arg Ser Glu Gln Ala Ala Ser Met
 340

<210> 21
 <211> 1515
 <212> DNA
 <213> Zea mays

<400> 21
 ggccccagcc gacgaggcga ggagcgtgca attccgtagc tgcaactgca acgaactccc 60
 tccctccctc gaccgtatcg cccgctgctc ctctatccct ttcttctgctgc tgctactacc 120
 ttaagctatc atggccttga tgctgctagc gcgcaacctg cgctcccgcc tccgcccacc 180
 gctcgccgcc gccgcggcgt tctcgctcggc cgcggcggag gcgagagagg cgatacggga 240
 cgggcccggg aacgactgga gccggcccga gatccaggcc gtctacgact caccgctcct 300
 cgacctctc tttcacgggg ctcagggtcca cagaaatgtc cataaattca gagaagtgca 360
 gcaatgcaca cttctttcaa tcaagactgg tggatgcagt gaagattggt cttactgtcc 420
 tcagtcataca agatacaaca ctggattgaa ggcccaaaaa ttgatgaaca aagatgctgt 480
 cttggaagca gcaaaaaagg caaaagagtc tgggagcacc cgtttttgca tgggagctgc 540
 atggagagaa accattggca ggaaatcaaa cttcaaccag attcttgaat atgtcaagga 600
 aataaggggt atgggcatgg aggtctgttg cacactaggc atgatagaga aacaacaagc 660
 tgaagaactc aagaaggctg gacttacagc atataatcat aacctagata catcaagaga 720
 gtattatccc aacattatta ccacaagatc atatgatgat agactgcaga ctcttgagca 780
 tgtccgtgaa gctggaataa gcatctgctc aggtggaatc attggtcttg gtgaagcaga 840
 ggaggaccgg gtagggttgt tgcataccct agctaccttg cctacacacc cagagagcgt 900
 tccattaat gcattggttg ctgtaaaagg cacacctctt gaggaccaga agcctgtaga 960
 gatctgggaa atgatccgca tgatcgccac tgctcggatc acgatgccaa aggcaatggt 1020
 gaggttttca gcaggccgag tacggttctc gatgccagaa caagcgtgtg gcttcctcgc 1080
 tggggccaac tccatctttg ccggcgagaa acttctcaca accgcaaaca acgactttga 1140
 tgcggaccag gcgatgttca agatccttgg cctgatcccc aaggctccaa gctttggcga 1200
 ggaagaggtg tctgcggcgg ctcccgcaga atccgagagg tctgagcaag ctgcttcgat 1260
 gtagaatata tacatatcat taccgattat ccgtatcacg gttggggcga aactagaact 1320
 accgtttag ctagagcatt ggattgtaga aaccacaaca tttcattatt ttgtaattgc 1380
 ttgagactga atgggggata cccatgtcgg gctagatcaa aaaaaaaaaa aaaaaaaaaa 1440
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaa 1515

<210> 22
 <211> 377
 <212> PRT
 <213> Zea mays

<400> 22
 Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
 1 5 10 15
 Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
 20 25 30
 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
 35 40 45
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
 50 55 60
 Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
 65 70 75 80
 Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
 85 90 95
 Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
 100 105 110

Asn Lys Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly
 115 120 125
 Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
 130 135 140
 Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly
 145 150 155 160
 Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln
 165 170 175
 Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
 180 185 190
 Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr
 195 200 205
 Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser
 210 215 220
 Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg
 225 230 235 240
 Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser
 245 250 255
 Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp
 260 265 270
 Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala
 275 280 285
 Arg Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val
 290 295 300
 Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn
 305 310 315 320
 Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe
 325 330 335
 Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala
 340 345 350
 Pro Ser Phe Gly Glu Glu Glu Val Ser Ala Ala Ala Pro Ala Glu Ser
 355 360 365
 Glu Arg Ser Glu Gln Ala Ala Ser Met
 370 375

<210> 23
 <211> 1439
 <212> DNA
 <213> Zea mays

<400> 23
 gcacgagggc gaggagcgtg caattccgta gctgcaacga actccctcga ccgtatcgcc 60
 cgctgctcct ctatcccttt cctgctgctg ctactacctt aagctatcac tatcatggcc 120
 ttgatgctgc tagcgcgcaa cctgcgctcc cgcctccgcc caccgctcgc cgccgccgcg 180


```

gcgttctcgt cggccgcggc ggaggcggag agggcgatac gggacggggc gcggaacgac 240
tggagccggc ccgagatcca ggccgtctac gactcaccgc tcctcgacct cctctttcac 300
ggggctcagg tccacagaaa tgtccataaa ttcagagaag tgcagcaatg cacacttctt 360
tcaatcaaga ctggtggatg cagtgaagat tgttcttact gtctcagtc atcaagatac 420
aacactggat tgaaggccca aaaattgatg aacaaatatg ctgtcttggg agcagcaaaa 480
aaggcaaaag agtctgggag caccggtttt tgcatgggag ctgcatggag agaaaccatt 540
ggcaggaaat caaacttcaa ccagattctt gaatatgtca aggaaataag gggatatggg 600
atggaggtct gttgcacact aggcattgata gagaaacaac aagctgaaga actcaagaag 660
gctggactta cagcatataa tcataaccta gatacatcaa gagagtatta tcccaacatt 720
attaccacaa gatcatatga tgatagactg cagactcttg agcatgtccg tgaagctgga 780
ataagcatct gctcaggtgg aatcattggg cttggtgaag cagaggagga ccgggtaggg 840
ttgttgcata ccctagctac cttgcctaca caccagaga gcgttcctat taatgcattg 900
gttgctgtaa aaggcacacc tcttgaggac cagaagcctg tagagatctg ggaaatgata 960
cgcatgatcg ccactgctcg gatcacgatg ccaaaggcaa tggtgaggct ttcagcagtc 1020
cgagtacggg tctcgatgcc agaacaagcg ctgtgcttcc tcgctggggc caactccatc 1080
tttgccggcg agaaacttct cacaaccgca aacaacgact ttgatgcgga ccaggcgatg 1140
ttcaagatcc ttggcctgat cccaaggct ccaagctttg gcgaggaaga ggcgtctgcg 1200
gcggctccca cagaatccga gaggtctgag caagctgctt cgatgtagaa tatatacata 1260
tcattaccga ttatccgtat cacggttggg gcgaaactag aactaccgtt gtagctagag 1320
cattggattg tagaaaccac aacatttcat tattttgtaa ttgcttgaga ctgaatgggg 1380
gatacccatg tcgggctaga tcaatggaca acttccacac aaaaaaaaaa aaaaaaaaaa 1439

```

<210> 24
 <211> 377
 <212> PRT
 <213> Zea mays

```

<400> 24
Met Ala Leu Met Leu Leu Ala Arg Asn Leu Arg Ser Arg Leu Arg Pro
 1              5              10              15

Pro Leu Ala Ala Ala Ala Ala Phe Ser Ser Ala Ala Ala Glu Ala Glu
      20              25              30

Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Ile
      35              40              45

Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
      50              55              60

Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
      65              70              75              80

Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
      85              90              95

Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
      100              105              110

Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly
      115              120              125

Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
      130              135              140

Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly
      145              150              155              160

Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln
      165              170              175

```

Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
180 185 190

Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr
195 200 205

Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser
210 215 220

Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg
225 230 235 240

Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser
245 250 255

Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp
260 265 270

Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala
275 280 285

Arg Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val
290 295 300

Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn
305 310 315 320

Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe
325 330 335

Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala
340 345 350

Pro Ser Phe Gly Glu Glu Glu Ala Ser Ala Ala Ala Pro Thr Glu Ser
355 360 365

Glu Arg Ser Glu Gln Ala Ala Ser Met
370 375

<210> 25

<211> 1477

<212> DNA

<213> Argemone mexicana

<400> 25

gcacgagcat	tcgagaaata	aagagctgta	aaatttttag	ggtttttctg	cataactcta	60
cactcgaagc	ttcatcaata	gaaatatcat	aaacagaaga	attcaaaatg	cttaaagttc	120
aatctttgag	agctcgtctt	cgacctttga	ttttcatttc	tacattttct	tctctctcat	180
catctttctt	ttcttcagct	gctgctgttc	aagcagaaag	aacgattaaa	gaagggtccaa	240
gaaacgattg	gagcagagat	gaaattaaat	cggtttatga	ttctccagtt	ctcgatcttc	300
tcttccatgc	agctcaagtc	catagacatg	ctcacaactt	caggggaagt	cagcaatgta	360
ctcttctctc	tgttaagaca	ggtgggtgca	gtgaagattg	ttcatattgt	ccacaatctt	420
ccaggatgta	cactggagtg	aaagcccaaa	agctgatgaa	caaggacgca	gttctgcagg	480
cagcagaaaa	ggcaaaggag	gcggttagta	cacgtttctg	catgggtgct	gcatggagag	540
atacagtggt	caggaagacc	aacttcaaac	agatcctcga	atatgtaaaa	gaaattcggg	600
gtatgggaat	ggaggtatgc	tgcactttag	gcatgatcga	gaagcagcaa	gctgtggaac	660
tcaagcagcg	tgggtctaca	gcttacaatc	ataatcttga	tacttcaaga	gagtattacc	720
ctaacatcat	caccacaaga	tcttacgatg	agcgcttgga	aactcttcag	ttcgtccggg	780
aagcagggat	caatgtctgc	tcaggaggaa	taatagggtc	aggagaagca	gaggaggatc	840

```

gagttggtct tttgcataca ctagcaacgc ttccttcaca tccagaaaagt gttcccatca 900
atgcattgct tgcagtcaaa ggcacacctc ttgaagatca gaagccagtt gaaatatggg 960
agatgattcg gatgattgct actgctagaa ttgtaatgcc aaaagcaatg gtcaggctat 1020
cagcaggctcg tgttcgatgt tccatgtccg agcaagctct ctgcttcctt gctggcgcca 1080
attccatctt cactggtgag aaactattga caactcccaa caatgatttt gacgcagatc 1140
aaatgatggt taagatttta gggctgacac caaaagctcc aaattttgac caaacatcaa 1200
catcttttoga agccgagaga tgtgaacaag aagcaactgc gtcatagttc ttgcttcgat 1260
gagattatat atttatccaa atgaagaaat tcccgtccac cgtgtaagct tctttctttt 1320
acatgaagtt tctttgtatg aattatgaaa cctccaaaat aagctatact atttataaca 1380
ggaagttact gctaaatttt caattccatg ggaaatctat tttatgaact caaaaaaaaaa 1440
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1477

```

<210> 26
 <211> 379
 <212> PRT
 <213> Argemone mexicana

```

<400> 26
Met Leu Lys Val Gln Ser Leu Arg Ala Arg Leu Arg Pro Leu Ile Phe
  1              5              10              15

Ile Ser Thr Phe Ser Ser Leu Ser Ser Ser Ser Ser Ser Ser Ala Ala
      20              25              30

Ala Val Gln Ala Glu Arg Thr Ile Lys Glu Gly Pro Arg Asn Asp Trp
      35              40              45

Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu
      50              55              60

Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu
      65              70              75              80

Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu
      85              90              95

Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys
      100             105             110

Ala Gln Lys Leu Met Asn Lys Asp Ala Val Leu Gln Ala Ala Glu Lys
      115             120             125

Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg
      130             135             140

Asp Thr Val Gly Arg Lys Thr Asn Phe Lys Gln Ile Leu Glu Tyr Val
      145             150             155             160

Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met
      165             170             175

Ile Glu Lys Gln Gln Ala Val Glu Leu Lys Gln Ala Gly Leu Thr Ala
      180             185             190

Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile
      195             200             205

Thr Thr Arg Ser Tyr Asp Glu Arg Leu Glu Thr Leu Gln Phe Val Arg
      210             215             220

```


aatctcagct ttgaagacac aaactccaac acttaaaaat aaatattgaa attattgatt 1500
 tttccctaaa aaaaaaaaaa aaaaaa 1526

<210> 28
 <211> 415
 <212> PRT
 <213> Glycine max

<400> 28
 Thr Lys Pro Asn Pro Lys His Lys Tyr Arg Cys Cys Leu Leu Ser Leu
 1 5 10 15
 Ser Cys Leu Tyr Ser Gln Ile Ser His Ser Phe Ser Val Val Ser Leu
 20 25 30
 Pro Asn Phe Glu Phe Glu Ser Lys Asn Met Phe Leu Ala Arg Pro Ile
 35 40 45
 Phe Arg Ala Pro Ser Leu Trp Ala Leu His Ser Ser Tyr Ala Tyr Ser
 50 55 60
 Ser Ala Ser Ala Ala Ala Ile Gln Ala Glu Arg Ala Ile Lys Glu Gly
 65 70 75 80
 Pro Arg Asn Asp Trp Ser Arg Asp Gln Val Lys Ser Ile Tyr Asp Ser
 85 90 95
 Pro Ile Leu Asp Leu Leu Phe His Gly Ala Gln Val His Arg His Ala
 100 105 110
 His Asn Phe Arg Glu Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr
 115 120 125
 Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys Pro Gln Ser Ser Lys Tyr
 130 135 140
 Asp Thr Gly Val Lys Gly Gln Arg Leu Met Asn Lys Glu Ala Val Leu
 145 150 155 160
 Gln Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met
 165 170 175
 Gly Ala Ala Trp Arg Asp Thr Leu Gly Arg Lys Thr Asn Phe Asn Gln
 180 185 190
 Ile Leu Glu Tyr Val Lys Asp Ile Arg Asp Met Gly Met Glu Val Cys
 195 200 205
 Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Val Glu Leu Lys Lys
 210 215 220
 Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr
 225 230 235 240
 Tyr Pro Asn Ile Ile Thr Thr Arg Thr Tyr Asp Glu Arg Leu Gln Thr
 245 250 255
 Leu Glu Phe Val Arg Asp Ala Gly Ile Asn Val Cys Ser Gly Gly Ile
 260 265 270

Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val Gly Leu Leu His Thr
275 280 285

Leu Ser Thr Leu Pro Thr His Pro Glu Ser Val Pro Ile Asn Ala Leu
290 295 300

Val Ala Val Lys Gly Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile
305 310 315 320

Trp Glu Met Ile Arg Met Ile Ala Thr Ala Arg Ile Val Met Pro Lys
325 330 335

Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg Phe Ser Met Pro Glu
340 345 350

Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu
355 360 365

Lys Leu Leu Thr Thr Pro Asn Asn Asp Phe Asp Ala Asp Gln Leu Met
370 375 380

Phe Lys Val Leu Gly Leu Leu Pro Lys Ala Pro Ser Leu His Glu Gly
385 390 395 400

Glu Thr Ser Val Thr Glu Asp Tyr Lys Glu Ala Ala Ser Ser Ser
405 410 415

<210> 29
<211> 1659
<212> DNA
<213> Glycine max

<400> 29
aaagagtgtgta tacagataga tttccaaact ccactcactc accactatgg cgactctcag 60
aacttcacctc tcacgatccc tcatcctcct tcgctccaat acccctaaac tcgcacctat 120
ctcttctctct gtctgctcttc aagttcaaaa gtcgagaaac tatggtaccg tatcatctgt 180
tctctctcaa gctacagaaa catcaagcac atcacctagt aaggatgtct accaagaagc 240
actcaacgca actgaacccc gcagcaattg gacaagagaa gaaatcaagg cgatctatga 300
taagccattg atggagttat gttgggggtgc tggtagtttg cacaggaaat tccatataacc 360
tggggctatt cagatgtgta cattgttgaa catcaagacg ggtggttgct cggaggattg 420
ttcttactgc gcccaatcat cccgctacca aaccggtctc aaagcctcca aaatggtctc 480
cgctgaatct gtctcgcag cgcggcgcat cgccaaagac aacggtagta cacgtttctg 540
catgggagcc gcgtggcgcg atatgcgtgg acgaaaaacc aatctcaaaa atgtcaaaac 600
aatgggttagc gagattcgcg gaatgggtat ggaagtatgt gtcacgcttg gtatgattga 660
tgcagagcaa gctcaggaac tcaaagaagc cggctcacg gcttataatc ataatgtgga 720
tacgtcgagg gatttctatc ccaagggtat cacgaccagg acttatgatg agagattgga 780
taccattaag aatgtgagag aggccggaat caatgtttgt acgggtggaa tcctcggatt 840
aggagaaaaat aagtctgacc atattggact tttggagacg gttgctacgt tgccttcgca 900
tccggaatca tttcctgtga acatgttagt ggctatcaaa ggaacaccac tggaaggaaa 960
caagaagggtg gaatttgaga atatgttgag aatgggtgag acggctagaa tcgtcatgcc 1020
taaaaccatc gtgcgttttg cagctggaag aggagaattg agcgaggaac aacaggtctt 1080
atgtttcatg gccggagcca atgcggtttt cacaggagaa acaatgttaa ccacaccagc 1140
cgttggatgg ggtgtcgatt ccgctggttt caacagatgg ggattaagac ccatggaaag 1200
tttcgagggtt gaagccttga agaacgataa acctgccact actaatcagg aaataccggt 1260
agaggcaagt aaggcagaga tgccagggtac agttgcttga ttgattgttt gatttggata 1320
cccagggcgt ttggtgcgct catcatctcg agtttttgca aggagattcg aacagtggaa 1380
gtgccgttgc gccaccattg ggattggcgt atcggaactga gattgactgt gccacgaaaa 1440
tgttttgccg tatcgtgtgt tgcacatctg tgggaattta gcgttggttg ttttggtttt 1500
ggttttgttt gatgtgagag aatgattgtt tagaagggga gaatgtatat acggaacagt 1560

agaatatatt cttgtctata agattatata ggataaatat atataagctt atcctcaaaa 1620
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1659

<210> 30
 <211> 417
 <212> PRT
 <213> Glycine max

<400> 30
 Met Ala Thr Leu Arg Thr Ser Leu Ser Arg Ser Leu Ile Leu Leu Arg
 1 5 10 15
 Ser Asn Thr Pro Lys Leu Ala Pro Ile Ser Ser Ser Val Arg Leu Gln
 20 25 30
 Val Gln Lys Ser Arg Asn Tyr Gly Thr Val Ser Ser Val Pro Pro Gln
 35 40 45
 Ala Thr Glu Thr Ser Ser Thr Ser Pro Ser Lys Asp Val Tyr Gln Glu
 50 55 60
 Ala Leu Asn Ala Thr Glu Pro Arg Ser Asn Trp Thr Arg Glu Glu Ile
 65 70 75 80
 Lys Ala Ile Tyr Asp Lys Pro Leu Met Glu Leu Cys Trp Gly Ala Gly
 85 90 95
 Ser Leu His Arg Lys Phe His Ile Pro Gly Ala Ile Gln Met Cys Thr
 100 105 110
 Leu Leu Asn Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
 115 120 125
 Ala Gln Ser Ser Arg Tyr Gln Thr Gly Leu Lys Ala Ser Lys Met Val
 130 135 140
 Ser Val Glu Ser Val Leu Ala Ala Ala Arg Ile Ala Lys Asp Asn Gly
 145 150 155 160
 Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Asp Met Arg Gly Arg
 165 170 175
 Lys Thr Asn Leu Lys Asn Val Lys Thr Met Val Ser Glu Ile Arg Gly
 180 185 190
 Met Gly Met Glu Val Cys Val Thr Leu Gly Met Ile Asp Ala Glu Gln
 195 200 205
 Ala Gln Glu Leu Lys Glu Ala Gly Leu Thr Ala Tyr Asn His Asn Val
 210 215 220
 Asp Thr Ser Arg Asp Phe Tyr Pro Lys Val Ile Thr Thr Arg Thr Tyr
 225 230 235 240
 Asp Glu Arg Leu Asp Thr Ile Lys Asn Val Arg Glu Ala Gly Ile Asn
 245 250 255
 Val Cys Thr Gly Gly Ile Leu Gly Leu Gly Glu Asn Lys Ser Asp His
 260 265 270

Ile Gly Leu Leu Glu Thr Val Ala Thr Leu Pro Ser His Pro Glu Ser
275 280 285

Phe Pro Val Asn Met Leu Val Ala Ile Lys Gly Thr Pro Leu Glu Gly
290 295 300

Asn Lys Lys Val Glu Phe Glu Asn Met Leu Arg Met Val Ala Thr Ala
305 310 315 320

Arg Ile Val Met Pro Lys Thr Ile Val Arg Leu Ala Ala Gly Arg Gly
325 330 335

Glu Leu Ser Glu Glu Gln Gln Val Leu Cys Phe Met Ala Gly Ala Asn
340 345 350

Ala Val Phe Thr Gly Glu Thr Met Leu Thr Thr Pro Ala Val Gly Trp
355 360 365

Gly Val Asp Ser Val Val Phe Asn Arg Trp Gly Leu Arg Pro Met Glu
370 375 380

Ser Phe Glu Val Glu Ala Leu Lys Asn Asp Lys Pro Ala Thr Thr Asn
385 390 395 400

Thr Glu Ile Pro Val Glu Ala Ser Lys Ala Glu Met Pro Gly Thr Val
405 410 415

Ala

<210> 31
<211> 1032
<212> DNA
<213> Triticum aestivum

<400> 31
gcacgagaga tgccgtccta gaagcagcaa aaaaggcaaa ggaggctggg agcaccgat 60
tttgcattgg agccgcatgg agagagacaa ttggcaggaa aacaaatttc aaccagattc 120
ttgaatatgt caaggacata agaggtatgg gcatggagggt ctgttgcacc ctgggcatgc 180
tagagaaaca acaagctgaa gaactcaaga aggctggact tacagcttat aatcataacc 240
tagatacatc aagagaatat taccccaaca ttatttctac aagatcgtac gatgatagat 300
tacagactct tcagcatgtc cgtgaagctg gaataagcgt ctgctcagggt ggaattattg 360
gtcttggaga ggcggaggaa gaccgtgtag ggctgttgca tacactggcc actttgcaa 420
cacaccacga gagcgttcct atcaatgcat tgattgctgt caaaggcacg cctcttcagg 480
atcagaagcc tgtagagata tgggaaatga tccgcatgat tgccagcgca cggatttgtga 540
tgccaaaggc aatggtgaga ctttcggcag ggagagtacg gttttccatg ccagaacaag 600
ctctctgctt tctcgtggg gccaaactcga tcttcgccgg tgaagagctc ctgacaactg 660
cgaacaatga ctttgatgcg gaccaggcaa tgttcaagat ccttggcctg attcccaagg 720
ctccaaactt tggcgtatga gaggtcatgg tagcagcacc cacggagaga tgtgagcaag 780
ccgctttgat gtaaaatgtc ggtatagatt ctcgagacca catccggtgc aaaactggca 840
ccattatctc cacctagagt tttgtactgt agagatcatg acattttata gtaacttcag 900
attcatcgaa ataaaaatagg gggttctctg caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 960
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
aaaaaaaaaa aa 1032

<210> 32
<211> 263
<212> PRT
<213> Triticum aestivum

<400> 32

Thr Arg Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly
1 5 10 15

Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
20 25 30

Lys Thr Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly
35 40 45

Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln
50 55 60

Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
65 70 75 80

Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Ser Thr Arg Ser Tyr
85 90 95

Asp Asp Arg Leu Gln Thr Leu Gln His Val Arg Glu Ala Gly Ile Ser
100 105 110

Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg
115 120 125

Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser
130 135 140

Val Pro Ile Asn Ala Leu Ile Ala Val Lys Gly Thr Pro Leu Gln Asp
145 150 155 160

Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Ser Ala
165 170 175

Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val
180 185 190

Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn
195 200 205

Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe
210 215 220

Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala
225 230 235 240

Pro Asn Phe Gly Asp Glu Glu Val Met Val Ala Ala Pro Thr Glu Arg
245 250 255

Cys Glu Gln Ala Ala Leu Met
260

<210> 33

<211> 378

<212> PRT

<213> Arabidopsis thaliana

<400> 33

Met Met Leu Val Arg Ser Val Phe Arg Ser Gln Leu Arg Pro Ser Val
1 5 10 15

Ser Gly Gly Leu Gln Ser Ala Ser Cys Tyr Ser Ser Leu Ser Ala Ala
 20 25 30
 Ser Ala Glu Ala Glu Arg Thr Ile Arg Glu Gly Pro Arg Asn Asp Trp
 35 40 45
 Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Leu Leu Asp Leu
 50 55 60
 Leu Phe His Gly Ala Gln Val His Arg His Val His Asn Phe Arg Glu
 65 70 75 80
 Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu
 85 90 95
 Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Ser Thr Gly Val Lys
 100 105 110
 Ala Gln Arg Leu Met Ser Lys Asp Ala Val Ile Asp Ala Ala Lys Lys
 115 120 125
 Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg
 130 135 140
 Asp Thr Ile Gly Arg Lys Thr Asn Phe Ser Gln Ile Leu Glu Tyr Ile
 145 150 155 160
 Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met
 165 170 175
 Ile Glu Lys Gln Gln Ala Leu Glu Leu Lys Lys Ala Gly Leu Thr Ala
 180 185 190
 Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Val Ile
 195 200 205
 Thr Thr Arg Ser Tyr Asp Asp Arg Leu Glu Thr Leu Ser His Val Arg
 210 215 220
 Asp Ala Gly Ile Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu
 225 230 235 240
 Ala Glu Glu Asp Arg Ile Gly Leu Leu His Thr Leu Ala Thr Leu Pro
 245 250 255
 Ser His Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly
 260 265 270
 Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg
 275 280 285
 Met Ile Gly Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu
 290 295 300
 Ser Ala Gly Arg Val Arg Phe Ser Met Ser Glu Gln Ala Leu Cys Phe
 305 310 315 320
 Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr
 325 330 335

Pro Asn Asn Asp Phe Asp Ala Asp Gln Leu Met Phe Lys Thr Leu Gly
 340 345 350
 Leu Ile Pro Lys Pro Pro Ser Phe Ser Glu Asp Asp Ser Glu Ser Glu
 355 360 365
 Asn Cys Glu Lys Val Ala Ser Ala Ser His
 370 375
 <210> 34
 <211> 363
 <212> PRT
 <213> Schizosaccharomyces pombe
 <400> 34
 Met Phe Thr Arg Thr Ile Arg Gln Gln Ile Arg Arg Ser Ser Ala Leu
 1 5 10 15
 Ser Leu Val Arg Asn Asn Trp Thr Arg Glu Glu Ile Gln Lys Ile Tyr
 20 25 30
 Asp Thr Pro Leu Ile Asp Leu Ile Phe Arg Ala Ala Ser Ile His Arg
 35 40 45
 Lys Phe His Asp Pro Lys Lys Val Gln Gln Cys Thr Leu Leu Ser Ile
 50 55 60
 Lys Thr Gly Gly Cys Thr Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser
 65 70 75 80
 Arg Tyr Asn Thr Gly Val Lys Ala Thr Lys Leu Met Lys Ile Asp Glu
 85 90 95
 Val Leu Glu Lys Ala Lys Ile Ala Lys Ala Lys Gly Ser Thr Arg Phe
 100 105 110
 Cys Met Gly Ser Ala Trp Arg Asp Leu Asn Gly Arg Asn Arg Thr Phe
 115 120 125
 Lys Asn Ile Leu Glu Ile Ile Lys Glu Val Arg Ser Met Asp Met Glu
 130 135 140
 Val Cys Val Thr Leu Gly Met Leu Asn Glu Gln Gln Ala Lys Glu Leu
 145 150 155 160
 Lys Asp Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg
 165 170 175
 Glu Tyr Tyr Ser Lys Ile Ile Ser Thr Arg Thr Tyr Asp Glu Arg Leu
 180 185 190
 Asn Thr Ile Asp Asn Leu Arg Lys Ala Gly Leu Lys Val Cys Ser Gly
 195 200 205
 Gly Ile Leu Gly Leu Gly Glu Lys Lys His Asp Arg Val Gly Leu Ile
 210 215 220
 His Ser Leu Ala Thr Met Pro Thr His Pro Glu Ser Val Pro Phe Asn
 225 230 235 240

Leu Leu Val Pro Ile Pro Gly Thr Pro Val Gly Asp Ala Val Lys Glu
 245 250 255
 Arg Leu Pro Ile His Pro Phe Leu Arg Ser Ile Ala Thr Ala Arg Ile
 260 265 270
 Cys Met Pro Lys Thr Ile Ile Arg Phe Ala Ala Gly Arg Asn Thr Cys
 275 280 285
 Ser Glu Ser Glu Gln Ala Leu Ala Phe Met Ala Gly Ala Asn Ala Val
 290 295 300
 Phe Thr Gly Glu Lys Met Leu Thr Thr Pro Ala Val Ser Trp Asp Ser
 305 310 315 320
 Asp Ser Gln Leu Phe Tyr Asn Trp Gly Leu Glu Gly Met Gln Ser Phe
 325 330 335
 Glu Tyr Gly Thr Ser Thr Glu Gly Glu Asp Gly Thr Phe Thr Leu Pro
 340 345 350
 Pro Lys Glu Arg Leu Ala Pro Ser Pro Ser Leu
 355 360

<210> 35
 <211> 375
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 35
 Met Met Ser Thr Ile Tyr Arg His Leu Ser Thr Ala Arg Pro Ala Leu
 1 5 10 15
 Thr Lys Tyr Ala Thr Asn Ala Ala Val Lys Ser Thr Thr Ala Ser Ser
 20 25 30
 Glu Ala Ser Thr Leu Gly Ala Leu Gln Tyr Ala Leu Ser Leu Asp Glu
 35 40 45
 Pro Ser His Ser Trp Thr Lys Ser Gln Leu Lys Glu Ile Tyr His Thr
 50 55 60
 Pro Leu Leu Glu Leu Thr His Ala Ala Gln Leu Gln His Arg Lys Trp
 65 70 75 80
 His Asp Pro Thr Lys Val Gln Leu Cys Thr Leu Met Asn Ile Lys Ser
 85 90 95
 Gly Gly Cys Ser Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser Arg Asn
 100 105 110
 Asp Thr Gly Leu Lys Ala Glu Lys Met Val Lys Val Asp Glu Val Ile
 115 120 125
 Lys Glu Ala Glu Glu Ala Lys Arg Asn Gly Ser Thr Arg Phe Cys Leu
 130 135 140
 Gly Ala Ala Trp Arg Asp Met Lys Gly Arg Lys Ser Ala Met Lys Arg
 145 150 155 160

Ile	Gln	Glu	Met	Val	Thr	Lys	Val	Asn	Asp	Met	Gly	Leu	Glu	Thr	Cys
165								170				175			
Val	Thr	Leu	Gly	Met	Val	Asp	Gln	Asp	Gln	Ala	Lys	Gln	Leu	Lys	Asp
180								185				190			
Ala	Gly	Leu	Thr	Ala	Tyr	Asn	His	Asn	Ile	Asp	Thr	Ser	Arg	Glu	His
195								200				205			
Tyr	Ser	Lys	Val	Ile	Thr	Thr	Arg	Thr	Tyr	Asp	Asp	Arg	Leu	Gln	Thr
210								215				220			
Ile	Lys	Asn	Val	Gln	Glu	Ser	Gly	Ile	Lys	Ala	Cys	Thr	Gly	Gly	Ile
225								230				235			
Leu	Gly	Leu	Gly	Glu	Ser	Glu	Asp	Asp	His	Ile	Gly	Phe	Ile	Tyr	Thr
245								250				255			
Leu	Ser	Asn	Met	Ser	Pro	His	Pro	Glu	Ser	Leu	Pro	Ile	Asn	Arg	Leu
260								265				270			
Val	Ala	Ile	Lys	Gly	Thr	Pro	Met	Ala	Glu	Glu	Leu	Ala	Asp	Pro	Lys
275								280				285			
Ser	Lys	Lys	Leu	Gln	Phe	Asp	Glu	Ile	Leu	Arg	Thr	Ile	Ala	Thr	Ala
290								295				300			
Arg	Ile	Val	Met	Pro	Lys	Ala	Ile	Ile	Arg	Leu	Ala	Ala	Gly	Arg	Tyr
305								310				315			
Thr	Met	Lys	Glu	Thr	Glu	Gln	Phe	Val	Cys	Phe	Met	Ala	Gly	Cys	Asn
325								330				335			
Ser	Ile	Phe	Thr	Gly	Lys	Lys	Met	Leu	Thr	Thr	Met	Cys	Asn	Gly	Trp
340								345				350			
Asp	Glu	Asp	Lys	Ala	Met	Leu	Ala	Lys	Trp	Gly	Leu	Gln	Pro	Met	Glu
355								360				365			
Ala	Phe	Lys	Tyr	Asp	Arg	Ser									
370								375							

<210>	36
<211>	12
<212>	PRT
<213>	